

GenCore version 4.5
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CM nucleic - nucleic search, using sw model

Run on: November 5, 2001, 14:28:35 : Search time 5173.87 Seconds
(without alignments)
4834.167 Million cell updates/sec

Title: US-09-593-316-3

Perfect score: 1617

Sequence: 1 ccgaagagccagccagctg.....attgaagagatattatct 1617

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: qb_ba1: *
2: qb_ba2: *
3: qb_ba3: *
4: qb_in1: *
5: qb_in2: *
6: qb_in3: *
7: qb_cm: *
8: qb_ov: *
9: qb_pat1: *
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94: qb_ro1: *
95: qb_ro2: *
96: qb_in4: *
97: qb_pr10: *
98: em_ba3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1617	100.0	1828	7 BOWGSTA
2	1617	100.0	1828	9 AR066344
3	1005	62.2	3684	7 AF221508
4	968.6	59.9	3640	7 AF221509
5	944.4	58.4	1412	9 AR066333
6	893.5	55.3	1269	7 PIGGCTA
7	866	53.6	1128	9 A69344
8	866	53.6	1128	9 A72021

Dp	781	GCTCATATGGTTTGGAAAGGCACTTCACACAGACGCCGTCTTAGACAATTATTATGCCAAG	846
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Dp	841	CAGAAAATACCGCTGCACCCTGAAGCGTTTTCCCGCGTGCGAGATACATTCAGCATTACTTG	900
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Dp	901	GAGAGCTTTTAAGCTGCTGATAAFAAGCACCTTCATGTGGGACCCAGCATCTTTAT	960
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Dp	961	ATCATGTTACATATATGTCTCCAGATATGCTTTGATATGATTTGGTCTCTGTGGCTCTTC	1020
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Dp	1021	AAACTGTTTAAGATCAAGCTTGAGAAGCGCTGGCAGGACATGACATGATGGCATGAG	1080
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Dp	1081	ACTATCGGAGGACACATGTGGTCCCATTCAGACATGACGTTGCTTTCTGCATG	1140
Qy	1141	gatttgaccaggatcttccaagacaagtttgaagtgaaaacctggagcgatcgttgcc	1200
Dp	1141	GATTTGACCAAGTCTTCTCAAACACAGTTTGAGGTGACACCTTGCGAGTCGGTGGCC	1200
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Dp	1261	GAGTCTCAGCATACATTCCTCTTCGTCGAAAGGGATTTATTATACCATACAGCCATTTT	1320
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DEFINITION	Sequence B from Patent US 5849991.	PAT	29-SEP-1999
ACCESSION	AR066334		
VERSION	AR066334.1	GI:5946550	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1828)		
AUTHORS	d'Aprile,A.J.F., Pearse,M.J., Robins,A.J., Crawford,R.J. and Rathjen,P.D.		
TITLE	Mice homozygous for an inactivated alpha.1,3-galactosyl transferase gene		
JOURNAL	Patent: US 5849991-A & 15-DPC-1998;		
DEPOSITOR	Local ion/quallifiers		
SOURCE	I. .1828		

[illegible]

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FILE	Trace: Homozygous for an inverted alpha-1-galactosyl transferase gene									
JOURNAL	Patient: US 584991-A 7 15-DEC-1998									
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ORIGIN	"unknown"									
Query Match	58-483	Score	944.4	Id%	92	Length	1412			
Post Local Similarity	87.3%	Prod. No.	5,207,184							
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RESULT 6
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LOCUS Sus scrofa alpha-1,3-galactosyltransferase mRNA, complete cds.
DEFINITION L36152.1 GI:642635
VERSION alpha-1,3-galactosyltransferase.
KEYWORDS Sus scrofa.
SOURCE Sus scrofa.
ORGANISM Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 1269)
AUTHORS Strahan,K.M., Gu.F., Prece,A.F., Gustavsson,L., Andersson,L. and
Gustavsson,K.
TITLE cDNA sequence and chromosome localization of pig alpha 1,3
JOURNAL Immunogenetics 41 (2-3), 101-105 (1995)
MEDLINE 95104914
FEATURES
Source location/Qualifiers
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95104914 /gene="GCTAL"
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CDS 16..1131
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Best local Similarity 87.4%; Prod. No. 1,4e-173;
Matches 1031; Conservative 0; Mismatches 129; Indels 20; Gaps 4;
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QY 575 accatcaagaaccccaagaatltggtgagcaagcattcaaaagatgattggtctcga 634
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DB 179 GCTGTTTACATATGAGACTACAGTTACCGACGAGAAAGAACCCCTATAGCTAGCA 248
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QY 522 tqtgtatttggaaatatatccacacccgaagccttltgtctgataaccatc 581
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QY 582 auaaaccgaagaat tggtaacacacacatcgaagagcagtgcttccgaagatgt 641
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DEFINITION alpha 1.3 galactosyltransferase [New World monkeys, marmoset
ACCESION S71333
VERSION S71333.1 GI:558051
KEYWORDS New World monkeys.
SOURCE Platyrrhini
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates.
REFERENCE Henton T.R., Macher B.A., Anzaki F. and Galili N.
AUTHORS Defining the minimal size of catalytically active primate alpha 1,3
TITLE galactosyltransferase: structure-function studies on the
recombinant truncated enzyme
JOURNAL Glycobiology 4 (2), 193-201 (1994)
MEDLINE 94331837
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gi150270] from the original journal article.
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Accession	Position	Sequence	Reference
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Qy	792	qttgqaaagqaaacttataaagaagatgactttagaacaattatattgcccagaagcagaanaattac	851
Dp	346	ATGGGAAGGCACTTACAAACAGAGACCGCTCTACAGTAATATTATATGCCAAACACGAAATATAC	405
Qy	852	ctgtgagcttacaatttttcccccctcggaataatcatatgaacattactttgaagagttctt	911
Dp	406	CTGTGGGCTTGACGGTATTTCATGCTGGAAATACATTGACCATTAACCTTGAGGAGATGCTT	465
Qy	912	aagctctgcttaataagaacttcatatggtgggcaccccacatccttllatctagtagtata	971
Dp	466	AATATCTGCAATATCATCTTCTCATAGTGTGGCCACAAGTATCTTTTACATCATAGTGGCA	525
Qy	972	taatgtctccagatgtgcttllatagaaqtlgggtgctctctagctgcttcaaaatgtttaa	103
Dp	526	TGATATCTCCGAGATGCGCTTTGATAGAGTGGGTGCTCTCGTTCCCTTTAAAGTGTGTA	585
Qy	1032	gatacaagcctcgagaagaagatggtcagaagacatcaagatgatagtcgatgaaatctcgggga	109
Dp	586	GATCAATATCCGAGAGAGAGGTGGCCAGAGCATCAGATATATCCGATGAAGACCATCGGGGGA	645
Qy	1092	gacacattgtgcccacatgcacagatagatgttaacttctcttctctgattgattgtaacca	115
Dp	646	GCAATCTCTGGCCCAATCTCAACACAGAGAGTGGACTTCTTCTTCGATTCACCTGGATCA	705
Qy	1152	ggtcttctcaagatgacttttggatgaaagacaccttggatcgatcgatgacagctataaagc	121
Dp	706	GGCTCTTCGAAACACACTTTGGGGGTGGAGACCTTGCGGCATCTGGTGGCTCAAGCTAACAGGC	765
Qy	1212	ctgagtgtacaagatcagatcccaatgacttcaacctacagaaagagcggaaagatctcgagc	127
Dp	766	CTGGTGTGTACAGGACACATCTCTACGAGTTCACTTACGAGAGCGCGAGAGAGTCCGACGC	825
Qy	1272	atacaattccctctgagaaagagaaatttcttatcccatgacgacatttttggaggaaacc	133
Dp	826	CTCAATTCTCGTTTGGCCAGCGGCAATTTTATATACACAGCGACCATTTTTCGGCGAACACC	885
Qy	1332	cactcagatctttaaactcagcccggaatgcttcaaaagatcctcagaagaagaanaa	139
Dp	886	CAGTCACTTCTTAAACATCATCTCAGGAGTCTCTTCAAGCGAATCTCTCAGAGCACAGAGAAA	945
Qy	1392	tgcataaagaagcccaatgatatgatagaagccatctaaacaagtalattctcttccaacaa	145
Dp	946	TGACATATGAAGCTGAGTGGCATATGTAAGGCAATCTAAACAGATATTCTCTTCAACAA	100
Qy	1452	acctactaaaatcttatacccttcaataatcctgtcgatattatcacataagctctaccctcgga	151
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Qy	1512	tattatccttatcgaagatgtctcttgagagaacaagaatataatgtagttagaataataat	157
Dp	1066	TATTAGCATTTTCTCAAGTATAGTGTGGCAGAAAAAAGATATTAATTTGTTAGAAATATACAT	112
Qy	1572	ctgact-----ttgtgccagatacttctgaaattggaagatataattct	1617
Dp	1126	CTGACTTTAAATTGTGGCAGCAATTTTCTGTAATTTGAAGAGATTAAGTCT	1176

JOURNAL	Patent: US 5821117-A 2 13-OCT-1998;
FEATURES	Location/Qualifiers
source	1..1423
BASE COUNT	413 a 305 c 348 g 357 t
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Query Match	50.7%; Score 819.4; DB %; Length 1423;
Best Local Similarity	84.3%; Pred. No. 2.5e-158;
Matches 1004; Conservative	0; Mismatches 131; Indels 56; Gaps
QY	444 agaagcagacatgagagagaaataatgatgtgcagagagaaagtgaattctgcactgct 503
DB	25 AGCTTCTGCCATCAGAGAAATAATGATGTGCAAGCAAGCTGTGCTGATGCT 84
QY	504 gattgtctcaactgtcatctttgtgttttggagatatacgaagccgagagatcttt 563
DB	85 GCTTGTCTCAACGTATGCTTGtGTTTGGGATAATCAATCAAC----- 127
QY	564 gtcttgatataaacccatcgaagaaaccgaagtttggtagcagagcatlcaaaagatg 623
DB	128 -----AGAAACCCAGAACT---TGGAGTACGTGCTCAGAGAGCTG 165
QY	624 gtgagcttcagatggttllaacatg-----gttaacatgaagagatgagat 674
DB	166 GTGCTTCTCCAGCTGCTTTATGCAATGGGATCACTACACTTACACGAAAGAGACCTAT 225
QY	675 aacgagaaagaaagaaagaagaacgaagagcga---aagaaagcttaagatgcagct 731
DB	226 AGGCACAGAAAGAGAACAAAGAAAGAGACACAGACAGAGAGCTTCCGCTAGTGGACTG 285
QY	732 gttaaccacatltaagccctcgagaggttggacatgacgaagtgagaaagcttcagat 791
DB	286 GTTTAATGCTGAAAGAACGCGTAAAGCTGCTGACCATTAACCAATGGAGAGCTCGAGT 345
QY	792 gtggagagcgaacttaagacagagacggtcttgaagaattatgacgaagaaattat 851
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QY	852 cgttcgagctgaagcttltgcgcgcgaagaalagatagaacatctagaagatctt 911
DB	406 CGTGGCGCTCACGGTCTTTTCTGCTGGAAATACATTGACATTACTTGGAGAGTCT 465
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DB	466 AATATCTGCAAAATATCACTACTTCATGTTGGCCCAAAAGTATCTTTTACATATATGTA 525
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DB	526 TGAATCTCCAGAGATGCTTGTGATAGAGCTGGGTGCTGCTCTTAAATCTGTGA 585
QY	1032 gatcaagcctcgagaaagagtgagagagatcgaagatgaatgagagaaagatctcagaa 1091
DB	586 GATCAAGATCCAGAGAGAGGTGGCCAGACATCAACATGATGCGATGAACACATCCGGA 645
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QY	1152 gactcttcagagacagtttggagtgagagacccctggagcagatctgtagccagatctcaaa 1211
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Db 309 CTTAGATATATATATGCAACAGAAAAATTACCGTGGCTTCTGCTGCTGCG 368
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Db 369 AAGATACATTGACCAATCTGAGAGGCTTCTTAATATCTGCAAAATACATATCTCATGGT 428
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Search completed: November 5, 2001, 14:29:11
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